Dkt. 57155-AA/JPW/ANX

1646
#8/13
Dm J
10-29-02

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Christophe P.G. Gerald, et al.   Examiner: J. F. Murphy

Serial No.: 09/866,248   Group Art Unit: 1646

Filed   : May 25, 2001

For   : DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors

> 1185 Avenue of the Americas
> New York, New York 10036
> October 15, 2002

Assistant Commissioner For Patents
Washington, D.C. 20231

Sir:

COMMUNICATION IN RESPONSE TO SEPTEMBER 13, 2002 OFFICE COMMUNICATION AND RAW SEQUENCE LISTING ERROR REPORT

This Communication is submitted in response to the September 13, 2002 Office Communication and Raw Sequence Listing Error Report issued by the United States Patent and Trademark Office in connection with the above-identified application. A copy of the Office Communication and Raw Sequence Listing Error Report is attached hereto as **Exhibit A**. The Office Communication provides a period of one month for filing a response. A response to this September 13, 2002 Office Communication is due on October 13, 2002.   However, since October 13, 2002 falls on a Sunday, a response filed on the next succeeding day which is not a Saturday, Sunday or Federal Holiday, i.e. Tuesday, October 15, 2002, is considered timely filed under 37 C.F.R. §1.7. Accordingly, this Communication is being timely filed.

The Office Communication indicates that the Communication filed August 10, 2001 is not fully responsive to the Office Communication mailed March 5, 2001 because the application does not fully comply with 37 C.F.R. 1.821 - 1.825.

Applicants: Christophe P.G. Gerald, et al.
Serial No.: 09/866,248
filed: May 25, 2001
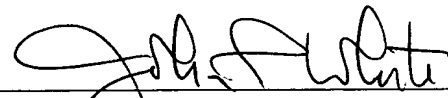
In response, applicants submit as **Exhibit B** hereto a corrected paper copy of the sequence listing which comply with 37 C.F.R. 1.821 - 1.825. Applicants also submit herewith a corrected formatted diskette containing a sequence listing in a computer readable form (CRF) as required by 37 C.F.R. §1.825(e). Further, applicants submit herewith a Statement in accordance with 37 C.F.R. §1.821(f) as **Exhibit C,** certifying that the computer readable form containing the nucleic acid and/or amino acid sequences as required by 37 C.F.R. §1.821(e) contains the same information which was submitted as the "Sequence Listing" and contains no new matter.

If a telephone interview would be of assistance in advancing prosecution of the subject application, applicants' undersigned attorney invite the Examiner to telephone him at the number provided below.
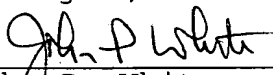
No fee is deemed necessary in connection with the filing of this Communication. If any other fee is required, authorization is hereby given to charge the amount of any such fee to Deposit Account No. 03-3125.

Respectfully submitted,

John P. White
Registration No. 28,678
Attorney for Applicants
Cooper & Dunham LLP
1185 Avenue of the Americas
New York, New York 10036
(212) 278-0400

I hereby certify that this correspondence is being deposited this date with the U.S. Postal Service with sufficient postage as first class mail in an envelope addressed to: Assistant Commissioner For Patents, Washington, D.C. 20231.

John P. White   10/15/02
John P. White   Date
Reg. No. 28,678

UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/866,248	05/25/2001	Christophe P.G. Gerald	1795/57155-AA JPW/BJA	6169

7590   09/13/2002

John P. White
Cooper & Dunham LLP
1185 Avenue of the Americas
New York, NY   10036

EXAMINER
MURPHY, JOSEPH F

ART UNIT	PAPER NUMBER
1646	

DATE MAILED: 09/13/2002

7

Please find below and/or attached an Office communication concerning this application or proceeding.

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office

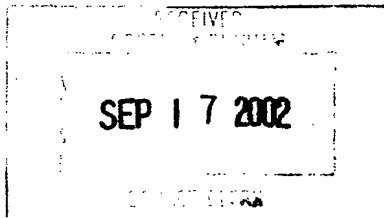Address: ASSISTANT COMMISSIONER FOR PATENTS
Washington, D.C. 20231

APPLICATION NO./ CONTROL NO.	FILING DATE	FIRST NAMED INVENTOR / PATENT IN REEXAMINATION	ATTORNEY DOCKET NO.

9/13/2002
1 mo: 10/13/2002
2 mos: 11/13/2002
3 mos: 12/13/2002
4 mos: 1/13/2003
5 mos: 2/13/2003
6 mos: 3/13/2003
SML

RECEIVED

SEP 17 2002

	EXAMINER

ART UNIT	PAPER
	7

DATE MAILED:

Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

Sequence Rules

The communication filed 8/10/2001 is not fully responsive to the Office communication mailed 3/5/2001 because the Application does not fully comply with 37 CFR 1.821-1.825. The sequence presented in claim 1 does not appear in the Sequence Listing. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Since the reply appears to be bona fide attempt to comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825), applicant is given a TIME PERIOD of ONE (1) MONTH from the mailing date of this communication within which to correct the deficiency so as to comply with the sequence rules (37 CFR 1.821 - 1.825) in order to avoid abandonment of the application under 37 CFR 1.821(g). EXTENSIONS OF THIS TIME PERIOD MAY BE GRANTED UNDER 37 CFR 1.136(a).

Advisory Information

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Joseph F. Murphy whose telephone number is 703-305-7245. The examiner can normally be reached on M-F 7:30-5:00. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Yvonne Eyler can be reached on 703-308-6564. The fax phone numbers for the organization where this application or proceeding is assigned are 703-305-3014 for regular communications and 703-308-0294 for After Final communications. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is 703-308-0196.

Joseph F. Murphy, Ph. D.
Patent Examiner Art Unit 1646
September 11, 2002

PTO-90C (Rev.3-98)

1646

RECEIVED
NOV 13 2001
TECH CENTER 1600/2900
#6

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY SYSTEMS BRANCH
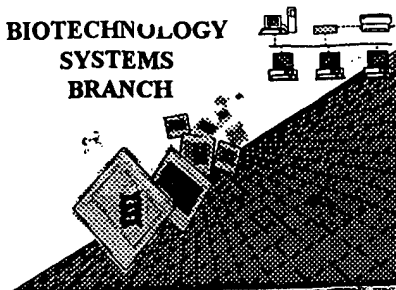
The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/866,248_

Source: _OIPE_

Date Processed by STIC: _6/19/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: *09/866 248*

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics / Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length — Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ___. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences (OLD RULES) — Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences (NEW RULES) — Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220> — Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

AMC – Biotechnology Systems Branch – 06/04/2001

RAW SEQUENCE LISTING   DATE: 06/19/2001
PATENT APPLICATION: US/09/866,248   TIME: 12:31:16

Input Set : A:\57155A.txt
Output Set: N:\CRF3\06192001\I866248.raw

p. 6

Does Not Comply
Corrected Diskette Needed

```
   5 <110> APPLICANT: Gerald, Christophe P.G.
   7         Jones, Kenneth A.
   9         Bonini, James A.
  11         Borowsky, Beth
  15 <120> TITLE OF INVENTION: DNA Encoding Mammalian Neuropeptide FF (NPFF) Receptors
  17         and Uses Thereof
  21 <130> FILE REFERENCE: 1795/57155-A
C--> 25 <140> CURRENT APPLICATION NUMBER: US/09/866,248
C--> 27 <141> CURRENT FILING DATE: 2001-05-25
  31 <150> PRIOR APPLICATION NUMBER: 09/161,113
  33 <151> PRIOR FILING DATE: 1998-09-25
  37 <160> NUMBER OF SEQ ID NOS: 42
  41 <170> SOFTWARE: PatentIn Ver. 2.0 - beta
  45 <210> SEQ ID NO: 1
  47 <211> LENGTH: 1410
  49 <212> TYPE: DNA
  51 <213> ORGANISM: Rattus norvegicus
  55 <400> SEQUENCE: 1
  57 acccttcctg ggccccagtc tacccgcttg aaggtgcccg cctcctttgg agagtgtccc 60
  59 ggagcagaca gtatggaggc ggagccctcc cagcctccca acggcagctg gcccctgggt 120
  61 cagaacggga gtgatgtgga gaccagcatg gcaaccagcc tcaccttctc ctcctactac 180
  63 caacactcct ctccggtggc agccatgttc atcgcggcct acgtgctcat cttcctcctc 240
  65 tgcatggtgg gcaacaccct ggtctgcttc attgtgctca gaaccggca catgcgcact 300
  67 gtcaccaaca tgtttatcct caacctggcc gtcagcgacc tgctggtggg catcttctgc 360
  69 atgcccacaa cccttgtgga caaccttatc actggttggc cttttgacaa cgccacatgc 420
  71 aagatgagcg gcttggtgca gggcatgtcc gtgtctgcat cggttttcac actggtggcc 480
  73 atcgctgtgg aaaggttccg ctgcatcgtg caccctttcc gcgagaagct gacccttcgg 540
  75 aaggcgctgt tcaccatcgc ggtgatctgg gctctggcgc tgctcatcat gtgtccctcg 600
  77 gcggtcactc tgacagtcac ccgagaggag catcacttca tgctggatgc tcgtaaccgc 660
  79 tcctacccgc tctactcgtg ctgggaggcc tggcccgaga agggcatgcg caaggtctac 720
  81 accgcggtgc tcttcgcgca catctacctg gtgccgctgg cgctcatcgt agtgatgtac 780
  83 gtgcgcatcg cgcgcaagct atgccaggcc cccggtcctg cgcgcgacac ggaggaggcg 840
  85 gtggccgagg gtggccgcac ttcgcgccgt agggcccgcg tggtgcacat gctggtcatg 900
  87 gtggcgctct tcttcacgtt gtcctggctg ccactctggg tgctgctgct gctcatcgac 960
  89 tatgggagc tgagcgagct gcaactgcac ctgctgtcgg tctacgcctt ccccttggca 1020
  91 cactggctgg ccttcttcca cagcagcgcc aacccccatca tctacggcta cttcaacgag 1080
  93 aacttccgcc gcggcttcca ggctgccttc cgtgcacagc tctgctggcc tccctgggcc 1140
  95 gcccacaagc aagcctactc ggagcggccc aaccgcctcc tgcgcaggcg ggtggtggtg 1200
  97 gacgtgcaac ccagcgactc cggcctgcca tcagagtctg gccccagcag cggggtccca 1260
  99 gggcctggcc ggctgccact gcgcaatggg cgtgtggccc atcaggatgg cccgggggaa 1320
 101 gggccaggct gcaaccacat gcccctcacc atcccggcct ggaacatttg aggtggtcca 1380
 103 gagaagggag ggccagtagt cctgtggccc                                    1410
 107 <210> SEQ ID NO: 2
 109 <211> LENGTH: 432
 111 <212> TYPE: PRT
 113 <213> ORGANISM: Rattus norvegicus
 117 <400> SEQUENCE: 2
```

RAW SEQUENCE LISTING   DATE: 06/19/2001
PATENT APPLICATION: US/09/866,248   TIME: 12:31:16

Input Set : A:\57155A.txt
Output Set: N:\CRF3\06192001\I866248.raw

```
119 Met Glu Ala Glu Pro Ser Gln Pro Pro Asn Gly Ser Trp Pro Leu Gly
121  1               5                10                15
125 Gln Asn Gly Ser Asp Val Glu Thr Ser Met Ala Thr Ser Leu Thr Phe
127             20                25                30
131 Ser Ser Tyr Tyr Gln His Ser Ser Pro Val Ala Ala Met Phe Ile Ala
133         35                40                45
137 Ala Tyr Val Leu Ile Phe Leu Leu Cys Met Val Gly Asn Thr Leu Val
139     50                55                60
143 Cys Phe Ile Val Leu Lys Asn Arg His Met Arg Thr Val Thr Asn Met
145 65                70                75                80
149 Phe Ile Leu Asn Leu Ala Val Ser Asp Leu Leu Val Gly Ile Phe Cys
151             85                90                95
155 Met Pro Thr Thr Leu Val Asp Asn Leu Ile Thr Gly Trp Pro Phe Asp
157            100               105               110
161 Asn Ala Thr Cys Lys Met Ser Gly Leu Val Gln Gly Met Ser Val Ser
163            115               120               125
167 Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Glu Arg Phe Arg Cys
169     130               135               140
173 Ile Val His Pro Phe Arg Glu Lys Leu Thr Leu Arg Lys Ala Leu Phe
175 145               150               155               160
179 Thr Ile Ala Val Ile Trp Ala Leu Ala Leu Leu Ile Met Cys Pro Ser
181             165               170               175
185 Ala Val Thr Leu Thr Val Thr Arg Glu Glu His His Phe Met Leu Asp
187             180               185               190
191 Ala Arg Asn Arg Ser Tyr Pro Leu Tyr Ser Cys Trp Glu Ala Trp Pro
193         195               200               205
197 Glu Lys Gly Met Arg Lys Val Tyr Thr Ala Val Leu Phe Ala His Ile
199     210               215               220
203 Tyr Leu Val Pro Leu Ala Leu Ile Val Val Met Tyr Val Arg Ile Ala
205 225               230               235               240
209 Arg Lys Leu Cys Gln Ala Pro Gly Pro Ala Arg Asp Thr Glu Glu Ala
211             245               250               255
215 Val Ala Glu Gly Gly Arg Thr Ser Arg Arg Arg Ala Arg Val Val His
217             260               265               270
221 Met Leu Val Met Val Ala Leu Phe Phe Thr Leu Ser Trp Leu Pro Leu
223         275               280               285
227 Trp Val Leu Leu Leu Leu Ile Asp Tyr Gly Glu Leu Ser Glu Leu Gln
229     290               295               300
233 Leu His Leu Leu Ser Val Tyr Ala Phe Pro Leu Ala His Trp Leu Ala
235 305               310               315               320
239 Phe Phe His Ser Ser Ala Asn Pro Ile Ile Tyr Gly Tyr Phe Asn Glu
241             325               330               335
245 Asn Phe Arg Arg Gly Phe Gln Ala Ala Phe Arg Ala Gln Leu Cys Trp
247         340               345               350
251 Pro Pro Trp Ala Ala His Lys Gln Ala Tyr Ser Glu Arg Pro Asn Arg
253         355               360               365
257 Leu Leu Arg Arg Arg Val Val Val Asp Val Gln Pro Ser Asp Ser Gly
259         370               375               380
263 Leu Pro Ser Glu Ser Gly Pro Ser Ser Gly Val Pro Gly Pro Gly Arg
```

RAW SEQUENCE LISTING   DATE: 06/19/2001
PATENT APPLICATION: US/09/866,248   TIME: 12:31:16

Input Set : A:\57155A.txt
Output Set: N:\CRF3\06192001\I866248.raw

```
265 385                     390                     395                     400
269 Leu Pro Leu Arg Asn Gly Arg Val Ala His Gln Asp Gly Pro Gly Glu
271                     405                     410                     415
275 Gly Pro Gly Cys Asn His Met Pro Leu Thr Ile Pro Ala Trp Asn Ile
277                     420                     425                     430
289 <210> SEQ ID NO: 3
291 <211> LENGTH: 200
293 <212> TYPE: DNA
295 <213> ORGANISM: Homo sapiens
299 <400> SEQUENCE: 3
301 gagccctccc agcctcccaa cagcagttgg cccctaagtc agaatgggac taacactgag 60
303 gccaccccgg ctacaaacct caccttctcc tcctactatc agcacacctc ccctgtggcg 120
305 gccatgttca ttgtggccta tgcgctcatc ttcctgctct gcatggtggg caacaccctg 180
307 gtctgtttca tcgtgctcaa                                            200
311 <210> SEQ ID NO: 4
313 <211> LENGTH: 66
315 <212> TYPE: PRT
317 <213> ORGANISM: Homo sapiens
321 <400> SEQUENCE: 4
323 Glu Pro Ser Gln Pro Pro Asn Ser Ser Trp Pro Leu Ser Gln Asn Gly
325   1               5                  10                  15
329 Thr Asn Thr Glu Ala Thr Pro Ala Thr Asn Leu Thr Phe Ser Ser Tyr
331             20                  25                  30
335 Tyr Gln His Thr Ser Pro Val Ala Ala Met Phe Ile Val Ala Tyr Ala
337         35                  40                  45
341 Leu Ile Phe Leu Leu Cys Met Val Gly Asn Thr Leu Val Cys Phe Ile
343      50                  55                  60
347 Val Leu
349  65
355 <210> SEQ ID NO: 5
357 <211> LENGTH: 1302
359 <212> TYPE: DNA
361 <213> ORGANISM: Homo sapiens
365 <400> SEQUENCE: 5
367 gccgacaggg ctcgccggga gaggttcatc atgaatgaga aatgggacac aaactcttca 60
369 gaaaactggc atcccatctg gaatgtcaat gacacaaagc atcatctgta ctcagatatt 120
371 aatattacct atgtgaacta ctatcttcac cagcctcaag tggcagcaat cttcattatt 180
373 tcctactttc tgatcttctt tttgtgcatg atgggaaata ctgtggtttg ctttattgta 240
375 atgaggaaca aacatatgca cacagtcact aatctcttca tcttaaacct ggccataagt 300
377 gatttactag ttggcatatt ctgcatgcct ataacactgc tggacaatat tatagcagga 360
379 tggccatttg aaacacgat gtgcaagatc agtggattgg tccagggaat atctgtcgca 420
381 gcttcagtct ttacgttagt tgcaattgct gtagataggt tccagtgtgt ggtctaccct 480
383 tttaaaccaa agctcactat caagacagcg tttgtcatta ttatgatcat ctgggtccta 540
385 gccatcacca ttatgtctcc atctgcagta atgttacatg tgcaagaaga aaaatattac 600
387 cgagtgagac tcaactccca gaataaaacc agtccagtct actggtgccg ggaagactgg 660
389 ccaaatcagg aaatgaggaa gatctacacc actgtgctgt ttgccaacat ctacctggct 720
391 cccctctccc tcattgtcat catgtatgga aggattggaa tttcactctt cagggctgca 780
393 gttcctcaca caggcaggaa gaaccaggag cagtggcacg tggtgtccag gaagaagcag 840
395 aagatcatta agatgctcct gattgtggcc ctgctttttta ttctctcatg gctgcccctg 900
```

```
397 tggactctaa tgatgctctc agactacgct gacctttctc caaatgaact gcagatcatc 960
399 aacatctaca tctacccttt tgcacactgg ctggcattcg gcaacagcag tgtcaatccc 1020
401 atcatttatg gtttcttcaa cgagaatttc cgccgtggtt tccaagaagc tttccagctc 1080
403 cagctctgcc aaaaaagagc aaagcctatg gaagcttatg ccctaaaagc taaaagccat 1140
405 gtgctcataa acacatctaa tcagcttgtc caggaatcta catttcaaaa ccctcatggg 1200
407 gaaaccttgc tttataggaa aagtgctgaa aaaccccaac aggaattagt gatggaagaa 1260
409 ttaaaagaaa ctactaacag cagtgagatt taaaaagagc ta                    1302
```

413 <210> SEQ ID NO: 6
415 <211> LENGTH: 420
417 <212> TYPE: PRT
419 <213> ORGANISM: Homo sapiens
423 <400> SEQUENCE: 6

```
425 Met Asn Glu Lys Trp Asp Thr Asn Ser Ser Glu Asn Trp His Pro Ile
427  1               5                  10                  15
431 Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp Ile Asn Ile
433              20                  25                  30
437 Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala Ala Ile Phe
439          35                  40                  45
443 Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met Gly Asn Thr
445      50                  55                  60
449 Val Val Cys Phe Ile Val Met Arg Asn Lys His Met His Thr Val Thr
451  65                  70                  75                  80
455 Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu Val Gly Ile
457              85                  90                  95
461 Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala Gly Trp Pro
463          100                 105                 110
467 Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu Val Gln Gly Ile Ser
469          115                 120                 125
473 Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val Asp Arg Phe
475      130                 135                 140
479 Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile Lys Thr Ala
481 145                 150                 155                 160
485 Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr Ile Met Ser
487          165                 170                 175
491 Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr Tyr Arg Val
493          180                 185                 190
497 Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp Cys Arg Glu
499          195                 200                 205
503 Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr Val Leu Phe
505      210                 215                 220
509 Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile Met Tyr Gly
511 225                 230                 235                 240
515 Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His Thr Gly Arg
517              245                 250                 255
521 Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys Gln Lys Ile
523          260                 265                 270
527 Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu Ser Trp Leu
529          275                 280                 285
533 Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp Leu Ser Pro
```

RAW SEQUENCE LISTING   DATE: 06/19/2001
PATENT APPLICATION: US/09/866,248   TIME: 12:31:16

Input Set : A:\57155A.txt
Output Set: N:\CRF3\06192001\I866248.raw

```
535     290                295                300
539 Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe Ala His Trp
541 305              310                315                320
545 Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr Gly Phe Phe
547           325                330                335
551 Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln Leu Gln Leu
553        340                345                350
557 Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Ala Leu Lys Ala Lys
559        355                360                365
563 Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln Glu Ser Thr
565     370                375                380
569 Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys Ser Ala Glu
571 385                390                395                400
575 Lys Pro Gln Gln Glu Leu Val Met Glu Glu Leu Lys Glu Thr Thr Asn
577           405                410                415
581 Ser Ser Glu Ile
583              420
589 <210> SEQ ID NO: 7
591 <211> LENGTH: 1293
593 <212> TYPE: DNA
595 <213> ORGANISM: Homo sapiens
599 <400> SEQUENCE: 7
601 atggagggg agccctccca gcctcccaac agcagttggc ccctaagtca gaatgggact 60
603 aacactgagg ccaccccggc tacaaacctc accttctcct cctactatca gcacacctcc 120
605 cctgtggcgg ccatgttcat tgtggcctat gcgctcatct tcctgctctg catggtgggc 180
607 aacaccctgg tctgtttcat cgtgctcaag aaccggcaca tgcatactgt caccaacatg 240
609 ttcatcctca acctggctgt cagtgacctg ctggtgggca tcttctgcat gcccaccacc 300
611 cttgtggaca acctcatcac tgggtggccc ttcgacaatg ccacatgcaa gatgagcggc 360
613 ttggtgcagg gcatgtctgt gtcggcttcc gttttcacac tggtggccat tgctgtggaa 420
615 aggttccgct gcatcgtgca ccctttccgc gagaagctga ccctgcggaa ggcgctcgtc 480
617 accatcgccg tcatctgggc cctggcgctg ctcatcatgt gtccctcggc cgtcacgctg 540
619 accgtcaccc gtgaggagca ccacttcatg gtggacgccc gcaaccgctc ctaccctctc 600
621 tactcctgct gggaggcctg gcccgagaag ggcatgcgca gggtctacac cactgtgctc 660
623 ttctcgcaca tctacctggc gccgctggcg ctcatcgtgg tcatgtacgc ccgcatcgcg 720
625 cgcaagctct gccaggcccc gggcccggcc cccgggggcg aggaggctgc ggacccgcga 780
627 gcatcgcggc gcagagcgcg cgtggtgcac atgctggtca tggtggcgct gttcttcacg 840
629 ctgtcctggc tgccgctctg ggcgctgctg ctgctcatcg actacgggca gctcagcgcg 900
631 ccgcagctgc acctggtcac cgtctacgcc ttccccttcg cgcactggct ggccttcttc 960
633 aacagcagcg ccaaccccat catctacggc tacttcaacg agaacttccg ccgcggcttc 1020
635 caggccgcct tccgcgcccg cctctgcccg cgccgtcgg ggagccacaa ggaggcctac 1080
637 tccgagcggc cggcggggct tctgcacagg cgggtcttcg tggtggtgcg gcccagcgac 1140
639 tccgggctgc cctctgagtc gggccctagc agtggggccc ccaggcccgg ccgcctcccg 1200
641 ctgcggaatg ggcgggtggc tcaccacggc ttgcccaggg aagggcctgg ctgctcccac 1260
643 ctgcccctca ccattccagc ctgggatatc tga                          1293
647 <210> SEQ ID NO: 8
649 <211> LENGTH: 430
651 <212> TYPE: PRT
653 <213> ORGANISM: Homo sapiens
657 <400> SEQUENCE: 8
```

<210> 9

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 9

~~gyrctwyryrr thwsgtgght gcc~~ ──────→ *see item 9 on Era Summary Sheet*   23

<210> 10

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer/probe

<400> 10

~~avnadngbrw avannanngg rtt~~ ──→ *item 9*   23

```
L:25 M:270 C: Current Application Number differs, Replaced Application Number
L:27 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:841 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:9
L:841 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:9
L:841 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:863 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:10
L:863 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:10
L:863 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
```